Amendments to the Claims:

1. (Currently Amended) A method for detecting a mutation in an HBV-derived nucleic acid target sequence in a sample, said method comprising:

subjecting the sample to denaturing conditions to yield single stranded forms of said target sequence;

contacting the denatured sample with a set of first and second primers having SEQ ID NO: 1 and SEQ ID NO: 2, respectively ~~wherein the first primer hybridizes under high stringency conditions to a region encoding the N-terminus of the major hydrophilic loop of HBV surface antigen and the second primer hybridizes under high stringency conditions to another region downstream from the C-terminus of the major hydrophilic loop of HBV surface antigen~~;

subjecting the sample to primer extension and amplification conditions to generate an amplified primer extension product; and

determining whether the amplified product comprises nucleic acid encoding major HBV surface antigen (SHBsAg) having a mutation at amino acid position 130, 131, 133 or 145, or having mutations at amino acid positions 130 and 145, 130 and 133, 131 and 145, or 133 and 145.

2-3 (Canceled)

4. (Previously presented) A method according to Claim 1, further comprising:

first subjecting the sample to reverse transcription conditions to yield single or double stranded cDNA molecules from HBV-derived mRNA.

5. (Previously presented) A method according to Claim 1 wherein the first primer is labeled with a reporter molecule capable of giving an identifiable signal and the second primer is labeled with a capturable moiety, or the first primer is labeled with a capturable moiety and the second primer is labeled with a reporter molecule capable of giving an identifiable signal.

6. (Previously presented) A method according to claim 5 wherein the primer labeled with a capturable moiety is immobilized to a solid support.

7-12. (Canceled)

13. (Currently Amended) A method according to Claim 5 wherein the capturable moiety is biotin and the reporter molecule is fluorescein or ~~Orcein~~ Texas Red.

14. (Previously presented) A method according to Claim 1 wherein the mutation at position 130 is from glycine to aspartic acid.

15. (Previously presented) A method according to Claim 1 wherein the mutation at position 131 is from threonine to asparagine.

16. (Previously presented) A method according to Claim 1 wherein the mutation at position 133 is from methionine to threonine.

17. (Previously presented) A method according to Claim 1 wherein the mutation at position 145 is from glycine to arginine.

18. (Previously presented) A method according to Claim 1 wherein the mutations at positions 130 and 145 are from glycine to aspartic acid at position 130, and from glycine to arginine at position 145.

19. (Previously presented) A method according to Claim 1 wherein the mutations at positions 130 and 133 are from glycine to aspartic acid at position 130, and from methionine to threonine at position 133.

20. (Previously presented) A method according to Claim 1 wherein the mutations at positions 131 and 145 are from threonine to asparagine at position 131, and from glycine to arginine at position 145.

21. (Previously presented) A method according to Claim 1 wherein the mutations at positions 130 and 145 are from methionine to threonine at position 133, and from glycine to arginine at position 145.

22. (Currently Amended) A method for evaluating whether a sample contains HBV that may have escaped immunological detection, said method comprising the steps of:

i) ~~contacting~~ mixing the sample with a set of first and second primers having SEQ ID NO: 1 and SEQ ID NO: 2, respectively ~~wherein the first primer hybridizes under high stringency conditions to a region encoding the N-terminus of the major hydrophilic loop of HBV surface antigen and the second primer hybridizes under high stringency conditions to another region downstream from the C-terminus of the major hydrophilic loop of HBV surface antigen~~;

ii) performing PCR on the mixture generated in step i) to generate an amplified primer extension product; ~~and~~

iii) determining whether the amplified product comprises nucleic acid encoding major HBV surface antigen (SHBsAg) having a mutation at amino acid position 130, 131, 133 or 145, or having mutations at amino acid positions 130 and 145, 130 and 133, 131 and 145, or 133 and 145~~, identification of~~; and

iv) identifying said mutation indicating that the sample contains HBV that may have escaped immunological detection.

23. (Canceled)

24. (Previously presented) A method according to Claim 22 wherein the mutation at position 130 is from glycine to aspartic acid.

25. (Previously presented) A method according to Claim 22 wherein the mutation at position 131 is from threonine to asparagine.

26. (Previously presented) A method according to Claim 22 wherein the mutation at position 133 is from methionine to threonine.

27. (Previously presented) A method according to Claim 22 wherein the mutation at position 145 is from glycine to arginine.

28. (Previously presented) A method according to Claim 22 wherein the mutations at positions 130 and 145 are from glycine to aspartic acid at position 130, and from glycine to arginine at position 145.

29. (Previously presented) A method according to Claim 22 wherein the mutations at positions 130 and 133 are from glycine to aspartic acid at position 130, and from methionine to threonine at position 133.

30. (Previously presented) A method according to Claim 22 wherein the mutations at positions 131 and 145 are from threonine to asparagine at position 131, and from glycine to arginine at position 145.

31. (Previously presented) A method according to Claim 22 wherein the mutations at positions 130 and 145 are from methionine to threonine at position 133, and from glycine to arginine at position 145.

32. (Currently Amended) A method for evaluating whether a sample contains HBV that may be resistant [be] to anti-HBV drug treatment, said method comprising the steps of:

i) contacting the sample with a set of first and second primers having SEQ ID NO: 1 and SEQ ID NO: 2, respectively ~~wherein the first primer hybridizes under high stringency conditions to a region encoding the N-terminus of the major hydrophilic loop of HBV surface antigen and the second primer hybridizes under high stringency conditions to another region downstream from the C-terminus of the major hydrophilic loop of HBV surface~~;

ii) performing PCR on the mixture generated in step i) to generate an amplified primer extension product; and

iii) determining whether the amplified product comprises nucleic acid encoding major HBV surface antigen (SHBsAg) having a mutation at amino acid position 130~~, 131, 133 or 145, or having mutations at amino acid positions 130 and 145, 130 and 133, 131 and 145, or 133 and 145~~, identification of said mutation indicating that the sample contains HBV that may be resistant to anti-HBV drug treatment.

33 (Previously presented) A method according to Claim 32 wherein the anti-HBV drug is lamivudine.

34. (Canceled).

35. (Previously presented) A method according to Claim 32 wherein the mutation at position 130 is from glycine to aspartic acid.

36-42. (Canceled)